

What is claimed is:

1. A substantially purified nucleic acid molecule comprising a nucleic acid sequence selected from SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or  
5 complements thereof or fragment of either.
2. A substantially purified maize transcription factor or soybean transcription factor or rice transcription factor or *Arabidopsis* transcription factor, or fragment thereof encoded by a first nucleic acid sequence which specifically hybridizes to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a  
10 complement of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478.
3. A substantially purified protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID  
15 NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 or fragment thereof.
4. A substantially purified protein or fragment thereof encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478.
- 20 5. A transformed cell or organism comprising a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof.
6. The transformed cell or organism according to claim 5, wherein said cell is  
25 a plant cell or plant.
7. The transformed cell or organism according to claim 6, wherein said cell or organism is a plant selected from the group consisting of cotton, wheat, maize and soybean.
8. A purified antibody or fragment thereof which is capable of specifically  
30 binding to a protein or fragment thereof, wherein the protein or fragment thereof

comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143.

9. A transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; (B) a structural nucleic acid molecule encoding a protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 or fragment thereof; and (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

10. The transformed plant according to claim 9, wherein said plant is maize.

11. The transformed plant according to claim 9 wherein said plant is soybean.

12. A transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to (B) a transcribed nucleic acid molecule with a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule encoding a protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in plant cells to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

13. A method for determining a level or pattern of a plant transcription factor in a plant cell or plant tissue comprising: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, the marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence selected from the

group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof or fragments of either, with a complementary nucleic acid molecule obtained from the plant cell or plant tissue, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue permits the detection of an mRNA for the enzyme; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue; and (C) detecting the level or pattern of the complementary nucleic acid, wherein the detection of the complementary nucleic acid is predictive of the level or pattern of the plant transcription factor.

14. A method for determining the level or pattern of a plant transcription factor in a plant cell or plant tissue comprising: (A) incubating under conditions permitting nucleic acid hybridization: a marker nucleic acid molecule, the marker nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof, with a complementary nucleic acid molecule obtained from a plant cell or plant tissue, wherein nucleic acid hybridization between the marker nucleic acid molecule, and the complementary nucleic acid molecule obtained from the plant cell or plant tissue permits the detection of said plant transcription factor; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue; and (C) detecting the level or pattern of the complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of the plant transcription factor.

15. A method of determining a mutation in a plant whose presence is predictive of a mutation affecting a level or pattern of a protein comprising the steps: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid, the marker nucleic acid selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having a nucleic acid sequence selected

from the group of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof and a complementary nucleic acid molecule obtained from the plant, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant permits the detection of a polymorphism whose presence is predictive of a mutation affecting the level or pattern of the protein in the plant; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism, wherein the detection of the polymorphism is predictive of the mutation.

16. A method of producing a plant containing an overexpressed protein comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region comprises a nucleic acid sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 or fragment thereof wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in overexpression of the protein; and (B) growing the transformed plant.

17. The method of producing a plant containing an overexpressed protein according to claim 16, wherein said plant is maize.

18. The method of producing a plant containing an overexpressed protein according to claim 16 wherein said plant is a soybean.

19. A method of producing a plant containing reduced levels of a plant transcription factor comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region

comprises a nucleic acid molecule encoding an amino acid sequence consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 or fragment thereof; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in co-suppression of the plant transcription factor; and (B) growing the transformed plant.

20. A method for reducing expression of a plant transcription factor in a plant comprising: (A) transforming the plant with a nucleic acid molecule, the nucleic acid molecule having an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule, wherein the exogenous promoter region is linked to a transcribed nucleic acid molecule having a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule having a nucleic acid sequence that encodes a plant transcription factor having an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 or fragments thereof and the transcribed strand is complementary to an endogenous mRNA molecule; and wherein the transcribed nucleic acid molecule is linked to a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and (B) growing the transformed plant.

21. The method for reducing expression of a plant transcription factor in a plant according to claim 20, wherein said plant is maize.

22. The method for reducing expression of a plant transcription factor in a plant according to claim 20, wherein said plant is a soybean.

23. A method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for the polymorphism to genetic material of a plant, wherein the nucleic acid molecule is

genetically linked to a nucleic acid molecule complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: through SEQ ID 13478 or complements thereof or fragment of either; and (B) calculating the degree of association between the polymorphism and the plant trait.

24. A method of isolating a nucleic acid that encodes a plant transcription factor or fragment thereof comprising: (A) incubating under conditions permitting nucleic acid hybridization, a first nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: through SEQ ID 13478 or complements thereof or fragment of either with a complementary second nucleic acid molecule obtained from a plant cell or plant tissue; (B) permitting hybridization between the first nucleic acid molecule and the second nucleic acid molecule obtained from the plant cell or plant tissue; and (C) isolating the second nucleic acid molecule.

25. An array comprising at least 30 different and separated target nucleic acid molecules immobilized on a solid support in a manner that complementary probe nucleic acid molecules can be hybridized thereto, wherein said target nucleic acid molecules have at least 20 consecutive nucleotides in a sequence selected from the group consisting of:

- (a) SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143;
- (b) sequences which are complements of (a);
- (c) sequences which have at least 60% identity to a sequence of (a) or (b);
- (d) sequences of molecules which hybridize to a sequence of (a) or (b) or (c);

26. An array according to claim 25 comprising at least 1000 distinct target nucleic acid molecules.

27. A method for preventing expression of a plant transcription factor in a plant cell comprising: (A) transforming the plant cell with a knockout construct, said construct comprising a nucleic acid molecule selected from the group consisting of SEQ

ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof or fragment of either.

28. A method for detecting an insertion event in a genome comprising: (A) preparing a DNA composition enhanced for a plurality of insertion junctions; (B) preparing at least a first detectable array comprising said DNA composition, wherein said preparing comprises directly or indirectly attaching said DNA composition to a solid support; (C) hybridizing a gene specific probe to said array, said gene specific probe detecting said insertion event from said first array and said gene specific probe comprising a nucleic acid sequence selected from SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof or fragment of either.

29. A method for selecting a plant having a trait, said method comprising the steps of: (A) obtaining genomic DNA from a plurality of plants; (B) analyzing genomic DNA from each of the plurality of plants to determine the presence or absence of a DNA marker that is genetically linked to a nucleic acid sequence complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof or fragment of either and (C) selecting said plant containing said DNA marker.